Docket No: M12C1FDF3D2

SEQUENCE LISTING

<110> Edwards, David L.
Hernstadt, Corinna
Wilcox, Edward R.
Wong, Siu-Yin

<120> Process for Altering the Host Range of Bacillus thuringiensis Toxins, and Novel Toxins Produced Thereby

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<141> 2001-12-27

<150> US 09/405,788
<151> 1999-09-27

<150> US 08/855,160
<151> 1997-05-13

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<151> 1995-04-10

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<151> 1993-07-27

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<151> 1992-11-23

<150> US 07/803,920
<151> 1991-12-06

<150> US 07/356,599
<151> 1989-05-24

<150> US 06/904,572
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Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
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Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
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Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
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His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
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Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
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Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Pro Val Gln Ile
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Gln Asp Asn Ser Val Pro Pro Arg Ala Gly Phe Ser His Arg Leu Ser
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Ala Gln Arg Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn
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Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr
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Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys
            660                 665                 670

Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
        675                 680                 685

Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly
    690                 695                 700

Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn
705                 710                 715                 720

Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu
                725                 730                 735

Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln
            740                 745                 750

Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile
        755                 760                 765
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Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser
    770                 775                 780

Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro
785                 790                 795                 800

Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser
                805                 810                 815

Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu
            820                 825                 830

Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp
        835                 840                 845

Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn
    850                 855                 860

Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg
865                 870                 875                 880

Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu
                885                 890                 895

Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala
            900                 905                 910

Leu Phe Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile
        915                 920                 925

Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala
    930                 935                 940

Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe
945                 950                 955                 960

Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala
                965                 970                 975

Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp
            980                 985                 990

Asn Val Lys Gly His Val Asp Val  Glu Glu Gln Asn Asn  Gln Arg Ser
        995                 1000                1005

Val Leu  Val Val Pro Glu Trp  Glu Ala Glu Val Ser  Gln Glu Val
    1010                1015                1020

Arg Val  Cys Pro Gly Arg Gly  Tyr Ile Leu Arg Val  Thr Ala Tyr
    1025                1030                1035

Lys Glu  Gly Tyr Gly Glu Gly  Cys Val Thr Ile His  Glu Ile Glu
    1040                1045                1050

Asn Asn  Thr Asp Glu Leu Lys  Phe Ser Asn Cys Val  Glu Glu Glu
    1055                1060                1065
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Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn
1070 1075 1080

Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr
1085 1090 1095

Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu
1100 1105 1110

Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe
1115 1120 1125

Asn Arg Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val
1130 1135 1140

Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
1145 1150 1155

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu
1160 1165 1170

Leu Leu Leu Met Glu Glu
1175

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tcgctaacgc aatttctttt gagtgaattt gttcccggtg ctggatttgt gttaggacta 180

gttgatataa tatggggaat ttttggtccc tctcaatggg acgcatttct tgtacaaatt 240

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gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360

cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420

cttacaaccg ctattcctct ttttgcagtt caaaattatc aagttcctct tttatcagta 480

tatgttcaag ctgcaaattt acatttatca gttttgagag atgtttcagt gtttggacaa 540

aggtggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt 600

ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggga 660

ccggattcta gagattgggt aaggtataat caatttagaa gagaattaac actaactgta 720

ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt 780

tcccaattaa caagagaaat ttatacaaac ccagtattag aaaattttga tggtagtttt 840

cgaggctcgg ctcagggcat agaaagaagt attaggagtc cacatttgat ggatatactt 900

aacagtataa ccatctatac ggatgctcat aggggttatt attattggtc agggcatcaa 960

ataatggctt ctcctgtagg gttttcgggg ccagaattca cttttccgct atatggaact 1020

atgggaaatg cagctccaca acaacgtatt gttgctcaac taggtcaggg cgtgtataga 1080

acattatcgt ccactttata tagaagacct tttaatatag ggataaataa tcaacaacta 1140

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agaggaagta cggatattac catccaagga ggcgatgacg tattcaaaga gaattacgtt 2160

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tccgtaccag ctgattatgc gtcagtctat gaagaaaaat cgtatacaga tggacgaaga 3360

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<211> 1177
<212> PRT
<213> Bacillus thuringiensis

<400> 6

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            20                  25                  30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
        35                  40                  45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
    50                  55                  60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65                  70                  75                  80
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Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
                85                  90                  95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
            100                 105                 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
        115                 120                 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
    130                 135                 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145                 150                 155                 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
                165                 170                 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
            180                 185                 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
        195                 200                 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
    210                 215                 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225                 230                 235                 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
                245                 250                 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
            260                 265                 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
        275                 280                 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
    290                 295                 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
305                 310                 315                 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
                325                 330                 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
            340                 345                 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
        355                 360                 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
    370                 375                 380
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Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385                 390                 395                 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asn Glu Ile Pro Pro Gln
                405                 410                 415

Asn Asn Asn Val Pro Pro Arg Gln Glu Phe Ser His Arg Leu Ser His
            420                 425                 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
        435                 440                 445

Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
    450                 455                 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465                 470                 475                 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
                485                 490                 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
            500                 505                 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
        515                 520                 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
    530                 535                 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
545                 550                 555                 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
                565                 570                 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
            580                 585                 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
        595                 600                 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
    610                 615                 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
625                 630                 635                 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
                645                 650                 655

Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
            660                 665                 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
        675                 680                 685
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Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
770 775 780

Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
900 905 910

Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
995 1000 1005

Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
1010 1015 1020

Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
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Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1040 1045 1050

Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
1055 1060 1065

Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
1070 1075 1080

Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
1085 1090 1095

Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
1100 1105 1110

Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg
1115 1120 1125

Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys
1130 1135 1140

Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
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Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu
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Leu Met Glu Glu
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<211> 3531
<212> DNA
<213> Bacillus thuringiensis

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gttgatataa tatggggaat ttttggtccc tctcaatggg acgcatttct tgtacaaatt 240

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gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360

cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420

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<211> 1177
<212> PRT
<213> Bacillus thuringiensis

<400> 8

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            20                  25                  30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
        35                  40                  45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
    50                  55                  60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65                  70                  75                  80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
                85                  90                  95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
            100                 105                 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
        115                 120                 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
    130                 135                 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145                 150                 155                 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
                165                 170                 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
            180                 185                 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
        195                 200                 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
    210                 215                 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225                 230                 235                 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
                245                 250                 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
            260                 265                 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
        275                 280                 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
    290                 295                 300
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Ile Tyr Thr Asp Ala His Lys Gly Glu Tyr Tyr Trp Ser Gly His Gln
305                 310                 315                 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
                325                 330                 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
            340                 345                 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
        355                 360                 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
    370                 375                 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385                 390                 395                 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
                405                 410                 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
            420                 425                 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
        435                 440                 445

Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
    450                 455                 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465                 470                 475                 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
                485                 490                 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
            500                 505                 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
        515                 520                 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
    530                 535                 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
545                 550                 555                 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
                565                 570                 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
            580                 585                 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
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Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
770 775 780

Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
900 905 910

Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
995 1000 1005

Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
1010 1015 1020

Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
1025 1030 1035

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1040 1045 1050

Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
1055 1060 1065

Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
1070 1075 1080

Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
1085 1090 1095

Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
1100 1105 1110

Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg
1115 1120 1125

Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys
1130 1135 1140

Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
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Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu
1160 1165 1170

Leu Met Glu Glu
1175

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<213> Artificial Sequence

<220>
<223> synthetic DNA fragment used to insert point mutations into pEW3 to create the plasmid pACB-1.

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gcccccgagg caagaattta gtcatcgatt aagccatgtt tcaatgttta gatctggctt 120

tagtaatagt agtgtaagta taataagagc t 151